Amendments to the Claims

Claim 1 (Original):   A method for genetically identifying an animal with respect to its potential

to reproductive longevity comprising:

obtaining a sample of genetic material from an animal; and

assaying for the presence of a polymorphism in the insulin-like growth factor 1 receptor

gene (IGF-1R), wherein the polymorphism is associated with reproductive longevity.

Claim 2 (Original):   The method of claim 1 wherein said polymorphism is selected from the

group consisting of: a single nucleotide polymorphism (SNP), a deletion, and an insertion.

Claim 3 (Original):   The method of claim 1 wherein the animal is selected from a group

consisting of: a mouse ,a pig, and a cow.

Claim 4 (Original):   The method of claim 1 wherein a step of assaying the polymorphism is

selected from the group consisting of: direct sequencing, restriction fragment length

polymorphism (RFLP) analysis, single-stranded conformation polymorphism (SSCP), PCR

amplification of specific alleles, amplification of DNA target by PCR followed by a mini-

sequencing assay, allelic discrimination during PCR, Genetic Bit Analysis, Pyrosequencing,

oligonucleotide ligation assay, and analysis of melting curves.

Claim 5 (Original):   The method of claim 4 wherein the step of assaying the polymorphism is

RFLP.

Claim 6 (Original):   The method of claim 4 wherein the step of assaying the polymorphism is SSCP.

Claim 7 (Original):   The method of claim 1 wherein the step of assaying for the presence of the polymorphism comprises the steps of:

digesting the genetic material with a restriction endonuclease that cleaves the gene in at

    least one place, wherein a particular restriction endonuclease pattern indicates the

    presence or absence of a polymorphism;

separating the fragments obtained from the digestion;

detecting a restriction pattern generated by the fragments; and

comparing the pattern with a second restriction pattern for the gene obtained by using the

restriction endonuclease, wherein the second restriction pattern is associated with reproductive

longevity.

Claim 8 (Original):   The method of claim 7 wherein said separation is by gel electrophoresis.

Claim 9 (Original):   The method of claim 7 further comprising:

amplifying the gene or a portion thereof which contains at least one polymorphism, prior to

digestion.

Claim 10 (Original):   The method of claim 9 wherein the amplification includes selecting a

forward and a reverse sequence primer capable of amplifying a region of the gene which contains

a polymorphism.

Claim 11 (Withdrawn):   The method of claim 1 wherein the polymorphism is identified as

an A to G nucleotide substitution at position 3876 of the gene.

Claim 12 (Withdrawn):   The method of claim 1 wherein the polymorphism is identified as a

G to A nucleotide substitution at position 331 of the gene.

Claim 13 (Withdrawn):   The method of claim 1 wherein the polymorphism is a 12 base pair

deletion at positions 3896-3907 of the gene.

Claim 14 (Withdrawn):   The method of claim 7 wherein the restriction endonuclease is

HpaII.

Claim 15 (Withdrawn):   The method of claim 7 wherein the restriction endonuclease DpnII.

Claim 16 (Withdrawn):   The method of claim 7 wherein the restriction endonuclease is

TaqI.

Claim 17 (Withdrawn):   The method of claim 7 wherein the restriction endonuclease is

Mn1I.

Claim 18 (Withdrawn):   The method of claim 7 wherein the restriction endonuclease is AvaII.

Claim 19 (Withdrawn):   The method of claim 10 wherein the forward primer is SEQ ID NO:8 and wherein the reverse primer is SEQ ID NO:9.

Claim 20 (Withdrawn):   The method of claim 10 wherein the forward primer is SEQ ID NO:10 and wherein the reverse primer is SEQ ID NO:11.

Claim 21 (Withdrawn):   The method of claim 10 wherein the forward primer is SEQ ID NO:12 and wherein the reverse primer is SEQ ID NO:13.

Claim 22 (Withdrawn):   The method of claim 10 wherein the forward primer is SEQ ID NO:14 and wherein the reverse primer is SEQ ID NO:15.

Claim 23 (Withdrawn):   The method of claim 10 wherein the forward primer is SEQ ID NO:16 and wherein the reverse primer is SEQ ID NO:17.

Claim 24 (Withdrawn):   The method of claim 10 wherein the forward primer is SEQ ID NO:18 and wherein the reverse primer is SEQ ID NO:19.

Claim 25 (Original): A method of screening animals to determine those more likely to have reproductive longevity, the method comprising:

obtaining a biological sample from an animal; and

assaying for the presence of a genotype in the IGF-1R gene, wherein the genotype is associated with reproductive longevity and characterized by a restriction fragment pattern, wherein said pattern when compared to a second restriction pattern is known to have or not have a desired polymorphic marker, the presence of said marker being indicative of an animal more likely to have reproductive longevity.

Claim 26 (Original): The method of claim 25 wherein the assaying step comprises amplifying the gene or a region thereof containing the marker with a forward and a reverse sequence primer.

Claim 27 (Withdrawn): The method of claim 26 wherein the forward primer is SEQ ID NO:8 and the reverse primer is SEQ ID NO:9.

Claim 28 (Withdrawn): The method of claim 26 wherein the forward primer is SEQ ID NO:10 and the reverse primer is SEQ ID NO:11.

Claim 29 (Withdrawn): The method of claim 26 wherein the forward primer is SEQ ID NO:12 and said reverse primer is SEQ ID NO:13.

Claim 30 (Withdrawn): The method of claim 26 wherein the forward primer is SEQ ID NO:14 and the reverse primer is SEQ ID NO:15.

Claim 31 (Withdrawn): The method of claim 26 wherein the forward primer is SEQ ID NO:16 and the reverse primer is SEQ ID NO:17.

Claim 32 (Withdrawn): The method of claim 26 wherein the forward primer is SEQ ID NO:18 and the reverse primer is SEQ ID NO:19.

Claim 33 (Withdrawn): The method of claim 25 wherein the marker is DpnII.

Claim 34 (Withdrawn): The method of claim 25 wherein the marker is HpaII.

Claim 35 (Withdrawn): The method of claim 25 wherein the marker is TaqI.

Claim 36 (Withdrawn): The method of claim 25 wherein the marker is Mn1I.

Claim 37 (Withdrawn): The method of claim 25 wherein the marker is AvaII.

Claim 38 (Withdrawn): The method of claim 33 wherein a G to A nucleotide substitution results in a restriction pattern characterized by a 328 nucleotide fragment, a 125 nucleotide fragment, and a 32 nucleotide fragment.

Claim 39 (Withdrawn):   The method of claim 34 wherein an A to G nucleotide substitution results in a restriction pattern characterized by a 373 nucleotide fragment, a 134 nucleotide fragment, and a 127 nucleotide fragment.

Claim 40 (Withdrawn):   The method of claim 34 wherein the deletion is characterized by a 12 bp fragment having SEQ ID NO:20 appearing once in the IGF-1R gene.

Claim 41 (Withdrawn):   The method of claim 35 wherein a G to A nucleotide substitution results in a restriction pattern characterized by a 135 nucleotide fragment and an 84 nucleotide fragment.

Claim 42 (Withdrawn):   The method of claim 36 wherein an G to C nucleotide substitution results in a restriction pattern characterized by a 137 nucleotide fragment, a 104 nucleotide fragment, a 55 nucleotide fragment, and an 11 nucleotide fragment.

Claim 43 (Withdrawn):   The method of claim 37 wherein an G to A nucleotide substitution results in a restriction pattern characterized by a 122 nucleotide fragment, an 81 nucleotide fragment, a 60 nucleotide fragment, and a 44 nucleotide fragment.

Claim 44 (Original):   The method of claim 25 wherein said animal is selected from the group consisting of: a pig and a mouse.

Claim 45 (Original): A method for screening animals to determine those more likely to exhibit favorable traits associated with reproductive longevity, said method comprising:

obtaining a genetic sample from an animal; and

detecting the presence or absence of at least one allele in the IGF-1R gene wherein the

presence of the allele is predictive of the animal having reproductive longevity.

Claim 46 (Withdrawn): The method of claim 45 wherein the allele is defined in intron 16 of the gene.

Claim 47 (Withdrawn): The method of claim 45 wherein the allele is defined in exon 21 at position 3876 of the gene.

Claim 48 (Withdrawn): The method of claim 45 wherein the allele is defined in exon 21 at positions 3896-3907 of the gene.

Claim 49 (Withdrawn): The method of claim 45 wherein the allele is defined at position 27 at the end of intron 16 of the gene.

Claim 50 (Withdrawn): The method of claim 45 wherein the allele is defined at position 73 at the end of intron 16 of the gene.

Claim 51 (Original): The method of claim 45 wherein the animal is selected from a group consisting of: a pig and a mouse.

Claim 52 (Withdrawn):   A method for determining the haplotype of the IGF-1R gene of an

animal comprising:

obtaining a genetic sample from an animal; and

analyzing the genetic sample for the presence of an IGF-1R gene A1D1, A1D2, or A2D1

        haplotype allele, wherein the haplotype effects reproductive performance

        or the ability to sustain stress factors.

Claim 53 (Withdrawn):   The method of claim 52 wherein the A1D1 allele is indicative of

having a favorable effect on lactation and pregnancy stress.

Claim 54 (Withdrawn):   The method of claim 52 wherein the A1D2 allele is indicative of

having a negative effect on reproductive performance.

Claim 55 (Withdrawn):   The method of claim 52 wherein the A2D1 allele is indicative of

reproductive longevity.

Claim 56 (Withdrawn):   The method of claim 52 wherein the animal is a mouse.

Claim 57 (Original):   A method for genotyping an animal for reproductive longevity, the method

comprising:

obtaining a sample of genetic material from an animal;

detecting a polymorphism in the IGF-1R gene of the animal;

determining whether the animal possesses a marker, wherein the marker is indicative of the

animal having two copies of allele 2.

Claim 58 (Original): The method of claim 57 wherein the step of detecting the polymorphism

comprises: digesting amplified nucleic acid with a restriction enzyme; and

separating the nucleic acid fragments according to size such that a restriction fragment

pattern is generated,

wherein the restriction fragment pattern generated is indicative of an animal reproductive

longevity.

Claim 59 (Original): The method of claim 57 wherein prior to digesting the nucleic acid with a

restriction enzyme, amplifying the nucleic acid with a forward primer and a reverse primer.

Claim 60 (Original): The method of claim 59 wherein the forward and reverse primer is SEQ ID

NO:21 and SEQ ID NO:22.

Claim 61 (Original): The method of claim 57 wherein the restriction enzyme is FokI.

Claim 62 (Original): The method of claim 58 wherein the restriction pattern characterized by a

295 nucleotide fragment, and a 55 nucleotide fragment.

Claim 63 (Original): The method of claim 57 wherein the marker is positively associated with

longevity.

Claim 64 (Original):   The method of claim 57 wherein the animal is a pig.

Claim 65 (Withdrawn):   A method for genetically identifying an animal comprising:

obtaining a sample of genetic material from an animal; and

assaying for the presence of a genotype in the IGF-1R gene sequence as set forth in SEQ

   ID NO:1 or a region thereof in the sample,

wherein the animal possesses a nucleic acid sequence having at least 95% sequence

   identity to SEQ ID NO:1 or a fragment thereof.

Claim 66 (Withdrawn):   The method of claim 65 wherein the polymorphism is identified by

a G to A nucleotide substitution in intron 16.

Claim 67 (Withdrawn):   The method of claim 65 wherein the polymorphism is identified by

an A to G nucleotide substitution in exon 21.

Claim 68 (Withdrawn):   The method of claim 65 wherein the polymorphism is identified as

a 12 bp deletion in exon 21.

Claim 69 (Withdrawn):   The method of claim 65 wherein the polymorphism is identified as

an insertion of a G nucleotide in intron 16 at position 176.

Claim 70 (Withdrawn):   The method of claim 65 wherein the animal is a mouse.

Claim 71 (Original):   A method for genetically identifying an animal comprising:

obtaining a sample of genetic material from an animal; and

assaying for the presence of a genotype in the IGF-1R gene sequence as set forth in SEQ

       ID NO:7 or a region thereof in the sample,

wherein the animal posses a nucleic acid sequence having at least 95% sequence

       identity to SEQ ID NO:7 or a fragment thereof.

Claim 72 (Withdrawn):   The method of claim 71 wherein said polymorphism is identified

as a G to A nucleotide substitution in intron 16.

Claim 73 (Withdrawn):   The method of claim 71 wherein said polymorphism is identified

as a G to C nucleotide substitution in intron 16.

Claim 74 (Withdrawn):   The method of claim 71 wherein said polymorphism is identified

as a G to A nucleotide substitution in exon 8.

Claim 75 (Original):   The method of claim 71 wherein the animal is a pig.

Claim 76 (Withdrawn):   The method of claim 65 wherein the polymorphism is an A to G

nucleotide substitution in exon 21 at position 3876.

Claim 77 (Withdrawn):   The method of claim 65 wherein the polymorphism is a 12 bp deletion in exon 21 at positions 3896-3907.

Claim 78 (Withdrawn):   The method of claim 71 wherein said polymorphism is a G to A nucleotide substitution at position 27 from the end of intron 16.

Claim 79 (Withdrawn):   The method of claim 71 wherein said polymorphism is a G to C nucleotide substitution at position 73 from the end of intron 16.

Claim 80 (Withdrawn):   A method for genetically identifying cattle with respect to its potential to reproductive longevity comprising:

obtaining a sample of genetic material from a cow; and

assaying for the presence of a polymorphism in the insulin-like growth factor 1 receptor gene (IGF-1R), wherein the polymorphism is associated with reproductive longevity.